












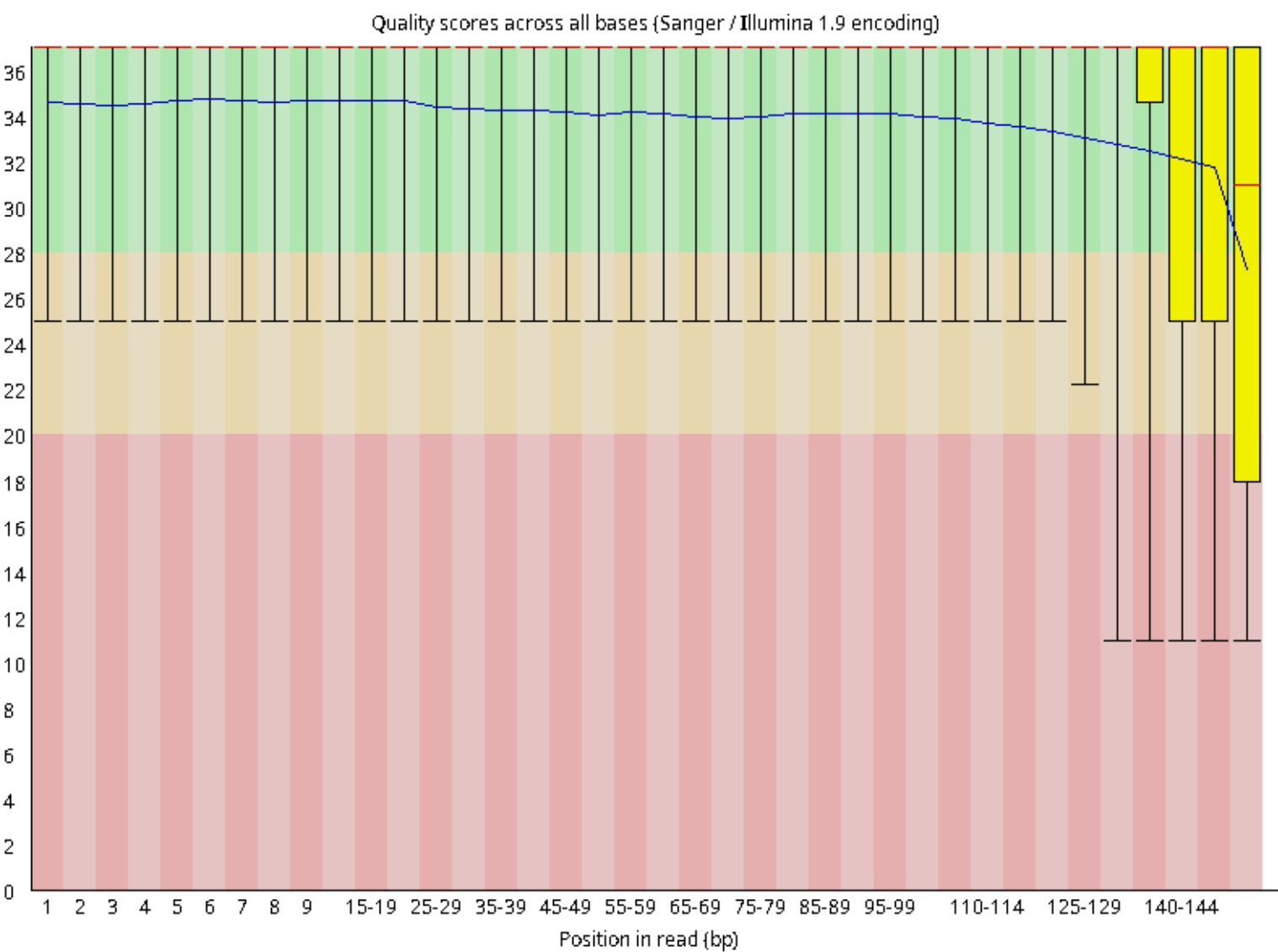
Summary

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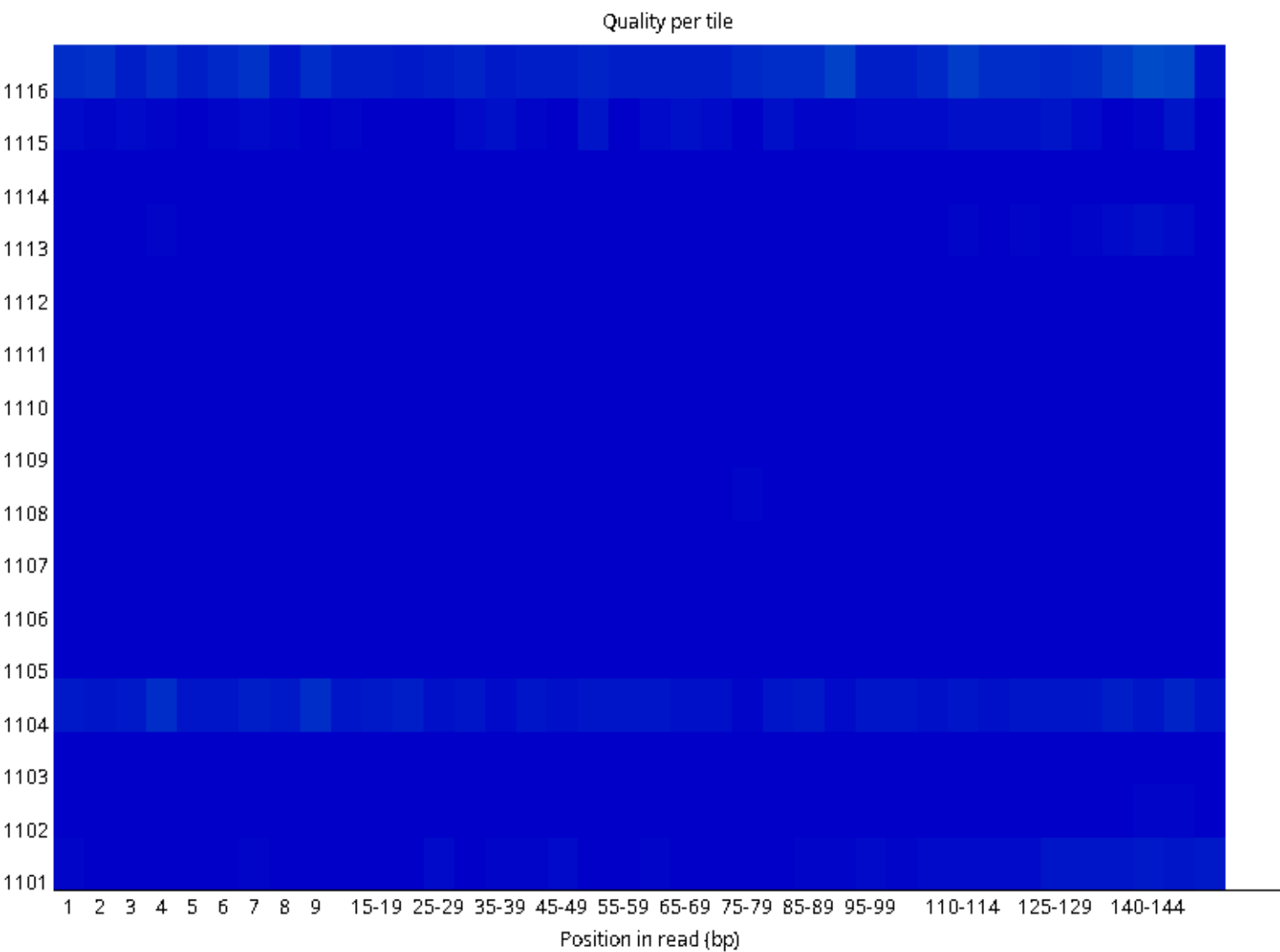
Basic Statistics

Measure	Value
Filename	SRR33784444_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	122837
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

✔ Per base sequence quality

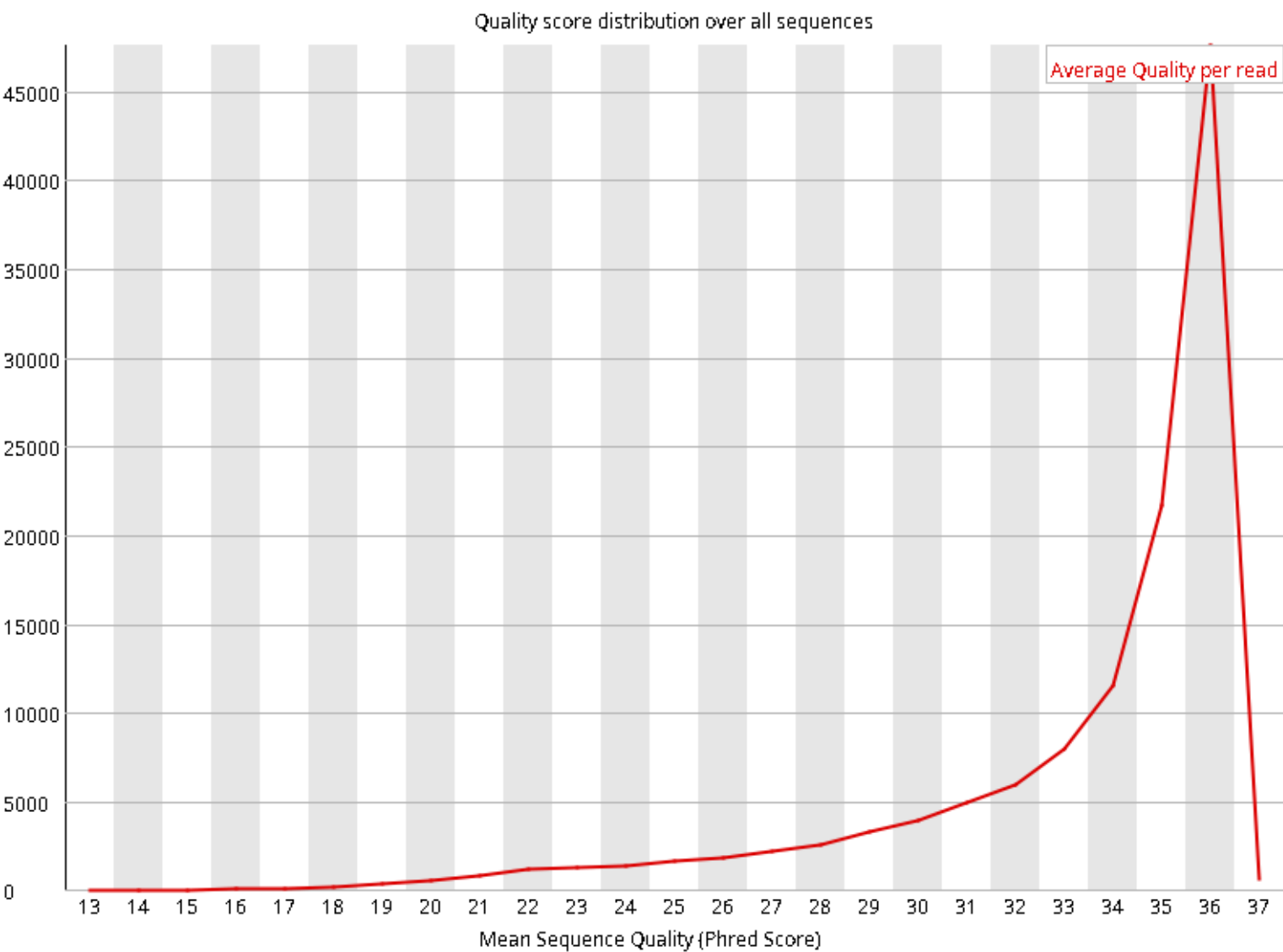


✔ Per tile sequence quality

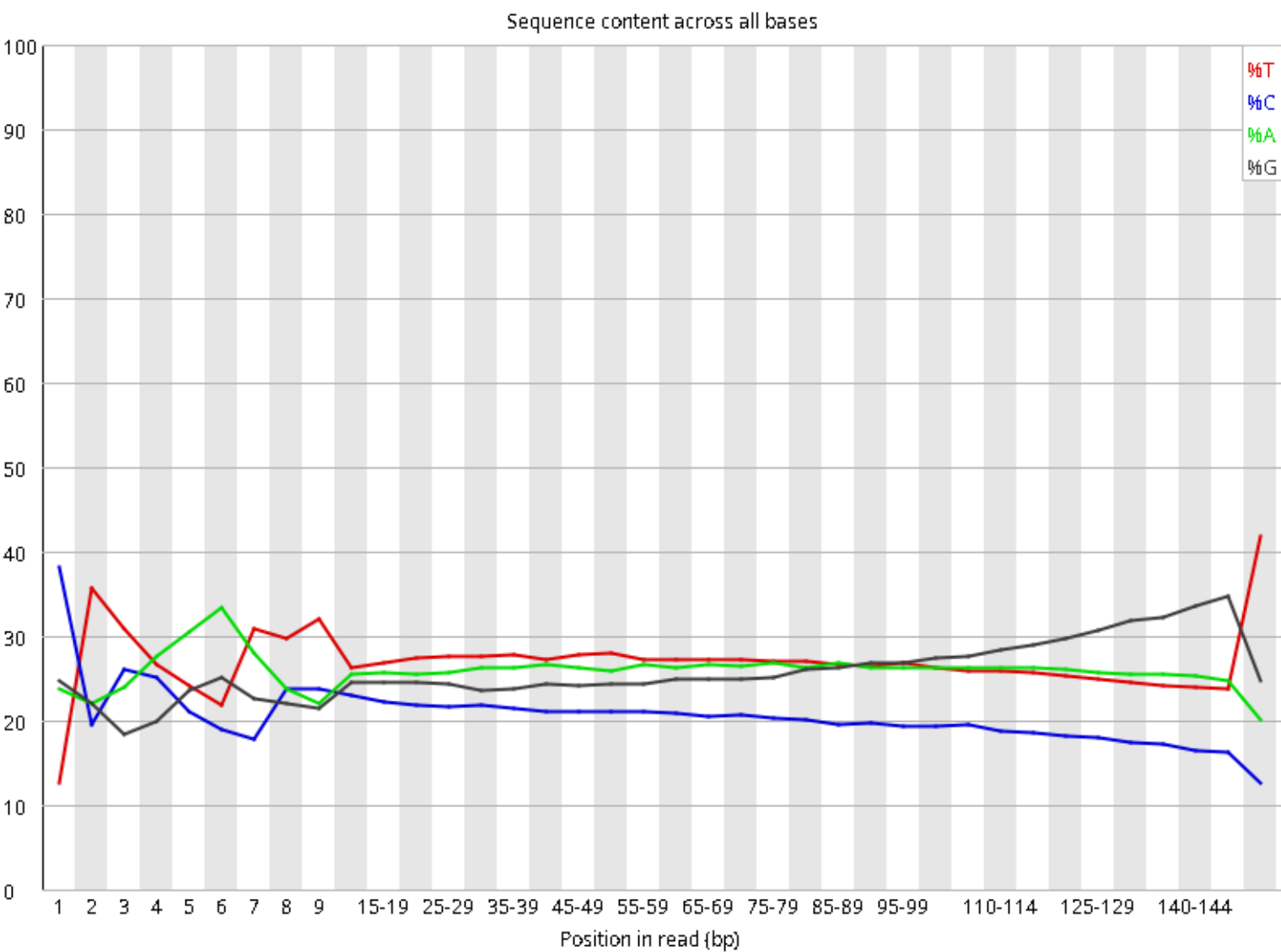




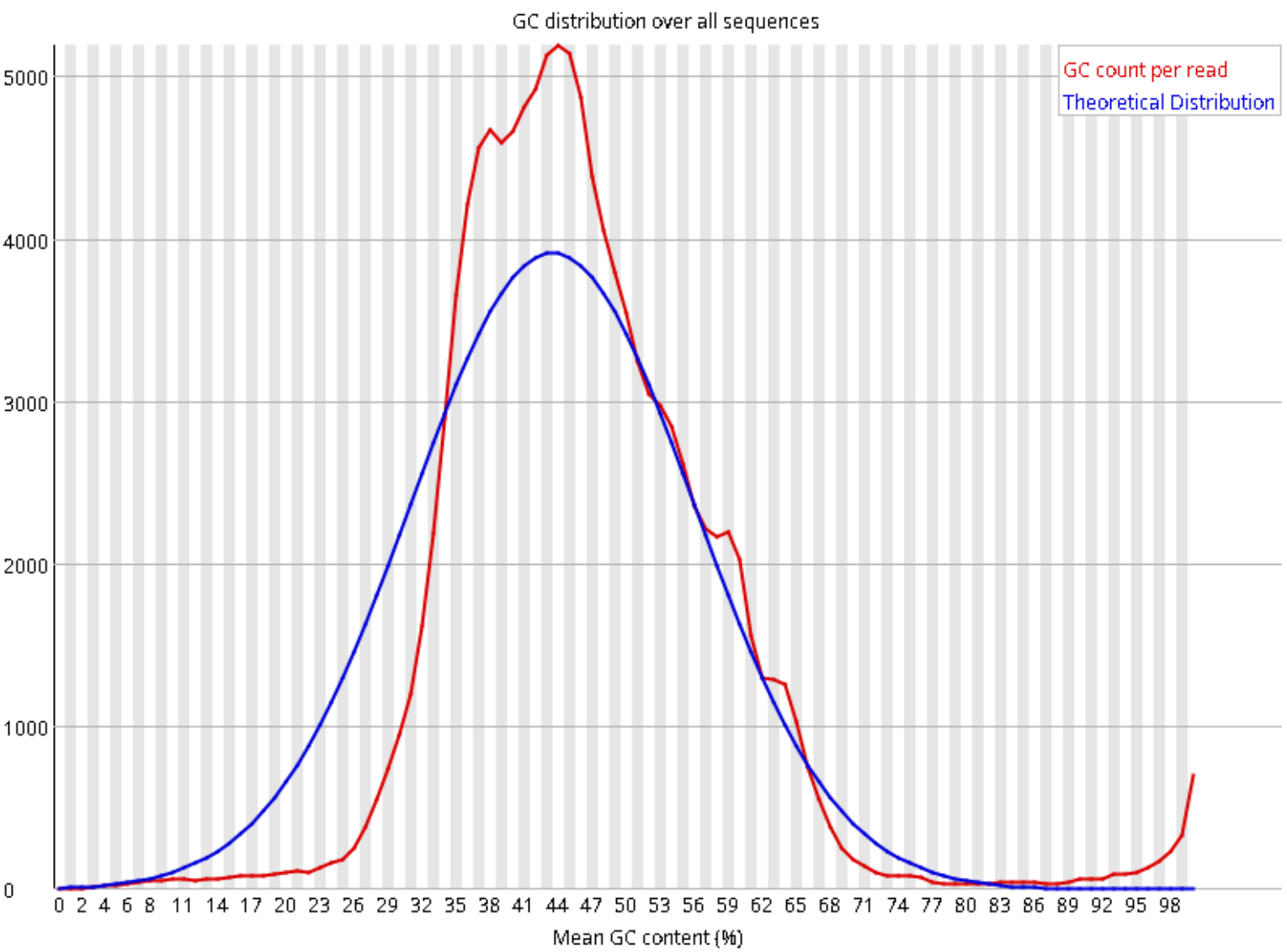
Per sequence quality scores



✖ Per base sequence content

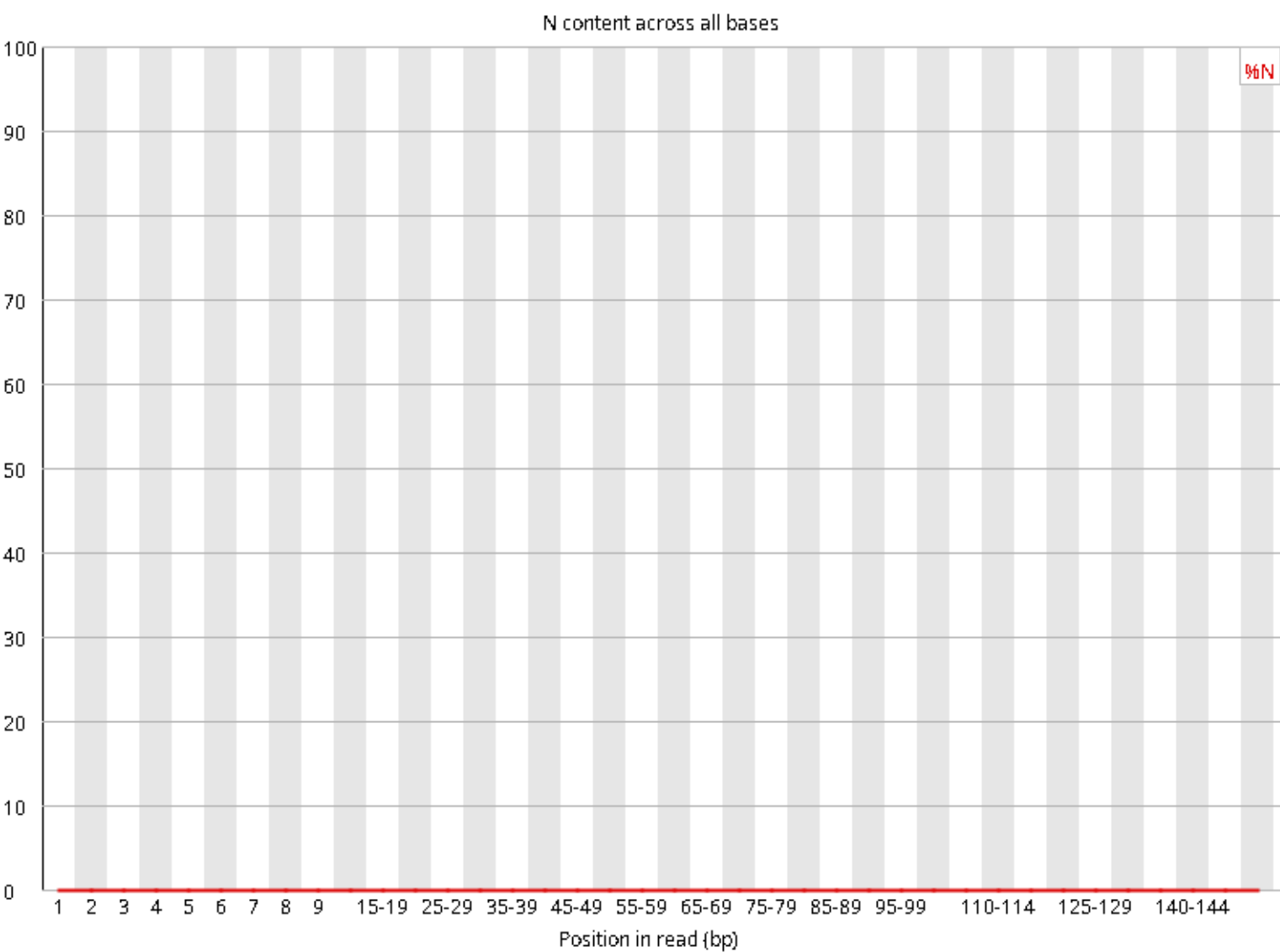


! Per sequence GC content

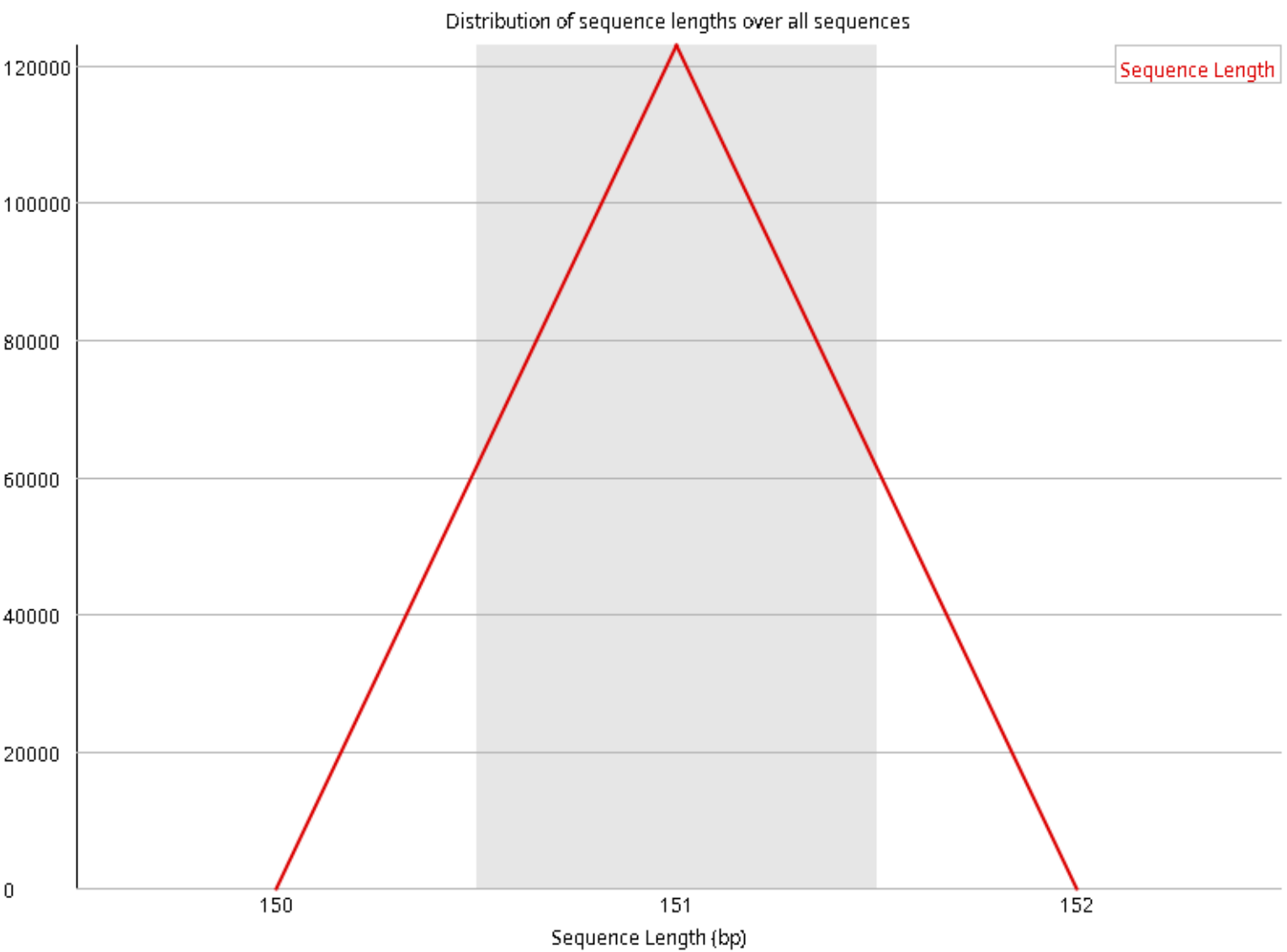




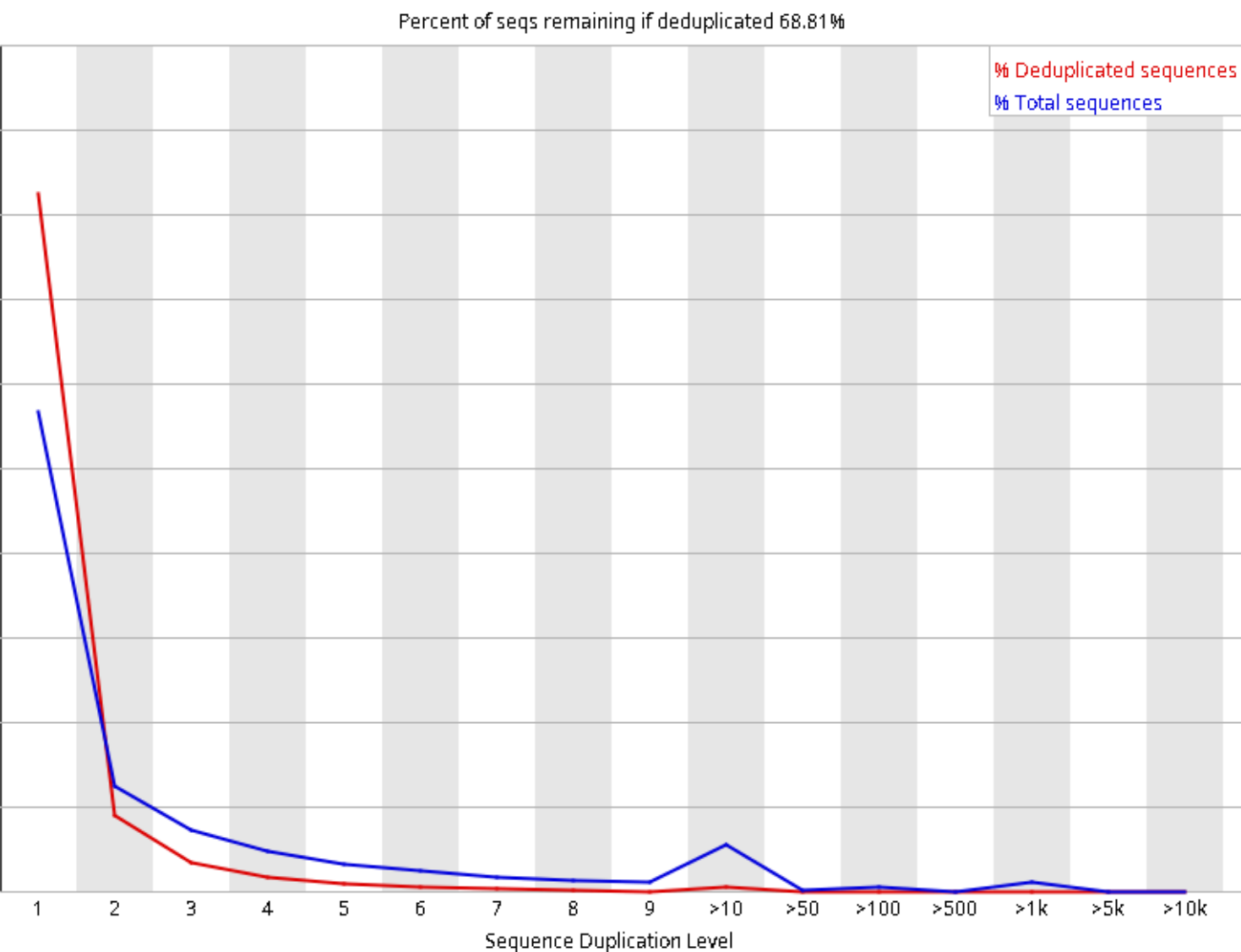
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

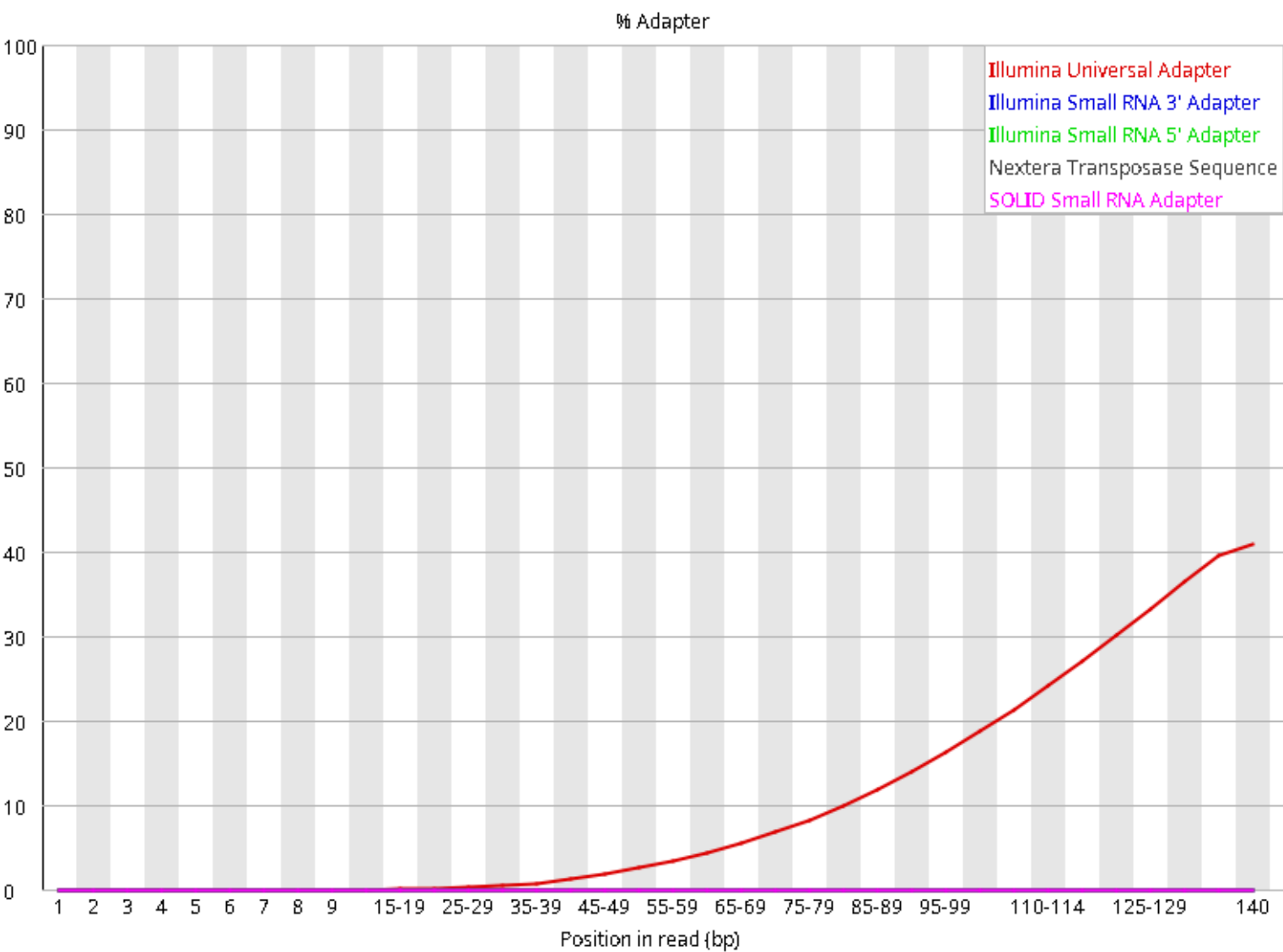


Overrepresented sequences

[illegible]



Adapter Content



Produced by [FastQC](#) (version 0.11.7)